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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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length: 2000000000
                                                                                                       SPTREMBL_17:*
1: Sp_archca:*
2: Sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-569-749-2
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Copyright (c) 1993 - 2000
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sp_plant:*
                                                                                                                                                                                 sp_archea:*
sp_bacteria:*
                                                                                                                                       sp_invertebrate:*
                                                                                          sp_organelle:*
                                                                                                                        sp_mammal:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                            sp_rodent:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

19	18	17	16	15	14	13	12	11	10	9	8	7	6	UI	4	w	N		Result No.
470	475.5	476	481.5	486	490	494	796.5	801.5	896.5	898.5	898.5	945.5	1138.5	1678	2185	2339	2625	2630	Score
14.3	14.5	14.5	14.7	14.8	15.0	15.1	24.3	24.5	27.4	27.4	27.4	28.9	34.7	51.2	66.7	71.4	80.1	80.3	Query
261	276	264	379	281	438	597	195	197	496	501	501	224	324	1140	602	610	589	589	Length
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## ALIGNMENTS

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A CONTRACTOR OF STANDARD STAND
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(*Cloning of cDNA for rat inhibitor of apoptosis protein 2.*;

tu submitted (sEp-199) to the EMBL/GenHank/DDBJ databases.

(*C -!* SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

BE HSSP; 013490; 10BH.

BIR INTERPOOZO: AAF04585.1; -.

BE FFAM: PF00639; CARD: 1.

BE FFAM: PF00639; CARD: 1.

BE FFAM: PF00639; CARD: 1.

BE SMART; SM00114; CARD: 1.

BE SMART; SM00184; RING; 1.
Query Match 80.3
Best Local Similarity 81.7
Matches 488; Conservative
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0902C6:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 17, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
1NHIBITOR OF APOPTOSIS PROTEIN 2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                  PROSITE: PS01282; BIR_REPEAT_1;
PROSITE: PS50143; BIR_REPEAT_2;
PROSITE: PS50209; CARD; 1.
Zinc-finger.
Zinc-finger.
SEQUENCE 589 AA; 66777 MW; 1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID-10116;
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                                               80.3%;
81.7%;
Score 2630; DB 11;
Pred. No. 1.3e-177;
53; Mismatches 48;
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Pfam; PF00619; CARD; 1.
Pfam; PF0061097; zf-C3HC4: 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; CARD; 1.
SMART; SM00114; RING; 1.
PR0SITE; PS01282; BIR_REPEAT_1: 1.
PR0SITE; PS0143; BIR_REPEAT_2; 3.
PR0SITE; PS01049; CARD; 1.
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OSESSE;
O1-MAR-2001 (TREMBLrel. 16, Created)
O1-MAR-2001 (TREMBLrel. 16, Last sequence update)
O1-UN-2001 (TREMBLRel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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              SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN: TISSUE-EMBRYONIC FIBROBLAST;
STRAIN-WHITE LEGHORN: TISSUE-EMBRYONIC FIBROBLAST;
MEDLINE-98038801; PubMed-9372964;
You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
You M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
Tou M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
Tou M., Ku P.-T., Hrdlickova R., Bose H.R. Jr.;
Tou M., Man M., Man
                                                                                                                                                                                                                                                                                   IAP1.
Gallus gallus (Chicken).
                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                          Archosauria;
                                                                                                                                                                                                                                                                                                                               PROTEINE)
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FUNCTION:
CELLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNLSMQTHAARMRTEMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDD
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                                                                                                                                                                                                                                               Aves;
                                                                                                                                                                                                                                               Neognathae;
                                                                                                                                                                                                                                                                  Chordata;
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81.6%;
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Pred.
                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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. NO. 2.9e-177;
ismatches 48;
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                     V-REL-TRANSFORMED
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                                                                                family,
                                                                                                                                                                                                                                               Phasianinae;
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SO THE TENERS OF THE TENERS OF

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Query Match 71.4
Best Local Similarity 71.4
Matches 437; Conservative
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Pfam; PF00653; CARD; 1.
Pfam; PF00097; xf-C3HC4 1.
Pfam; PF00097; xf-C3HC4 1.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: CONTAINS A C3HC4-CLASS EMBL; AF008592; AAB88044.1; -. HSSP; Q13490; 1QBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01282; BIR_REPEAT_1;
PROSITE; PS50143; BIR_REPEAT_2;
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC -1- SIMILARITY: MEMBER OF THE LAP FAMILY.
-1- SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION APOPTOSIS PROTEIN REPEAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY IN TESTIS. BRAIN, AND SKELETAL MUSCLE.
INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMAT PROCESS.
                                                                                                                                                                                                                                                                                                                                                       TSPMRNSFAHSLSPTLEHSSLFSGSYSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEAR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDKVKCFSCGLVLDNWQPGDNAMEKHKQYYPSCSFVQNMLSLNNLGLSTHSAFSPLVASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDKVKCFCCGLMLDNWKLGDSPIQKHKQLYPSCSFIQNLVSA-SLG-ST------SKN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIMDSSPLLASVMKQNAHCGELKYDLSCELYRMSTFSTFPVNVPVSERRLARAGFYYTGV 61
                                                                                      VNDIVSALLNAEDEKREEEKEKQAEEMASDDLSLIRKNEMALFQQLTCVLPILDNLLKAN
                                                                                                                                             VDENMD-PIIHFEPGESPSEDAIMMNTPVVKAALEMGFSRRLIKQTVQSKILATEENYKT
                                                                                                                                                              GEENADPPIIHFGPGESSSEDAVMMNTPVVKSALEMGENRDLVKQTVQSKILTTGENYKT
                                                                                                                                                                                                               FCCDGGLRCWESGDDPWIEHAKWFPRCEYLLRVKGGEFVSQVQARFPHLLEQLLSTSDTP
                                                                                                                                                                                                                                FCCDGGLRCWESGDDPWVEHAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTSDTT
                                                                                                                                                                                                                                                                                     PFVENLMRDQPSFNVSNVTMQTHEARVKTFINWPTRIPVQPEQLADAGFYYVGRNDDVKC
                                                                                                                                                                                                                                                                                                                       PFLENSL-ETLRFSISNLSMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKC
                                                                                                                                                                                                                                                                                                                                                                                                                               LSPSLRSM--TLSPSFEQVGYFSGSFSSFPQDPVTTRAAEDLSHLRSKLHNPSMSTEEAR
                                                                        VNDLVSDLLTAEDEKREEEKERQFEEVASDDLSLIRKNRMALFQRLTSVLPTLGSLLSAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; IPR001370; BIR.
; IPR001315; CARD.
; IPR001841; Znf_ring.
000653; BIR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger;
30 97
176 242
262 329
563 597
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71.4%;
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BIR REPEAT 1.
BIR REPEAT 2.
BIR REPEAT 3.
C3HC4-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2339; DB 13;
Pred. No. 4.7e-157;
8; Mismatches 81;
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"Clooing and Characterization of the Rat Homologs of the In Propersis Protein 1, 2, and 3 Genes.";

Submitted (SEP-1999) to the EMBI,/GenBank/DDBJ databases.

-1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER. R. EMBI, AR183430; AM622970.1; -.

R InterPro: IPR001315; CARD. InterPro: IPR001315; CARD. InterPro: IPR001315; CARD. InterPro: IPR001815; CARD. InterPro: IPR00181; Znf_ring. R. Finger Pr00639; BIR; 3.

R Pfam; PP00639; ARD: 1.

R Pfam; PP00097; zf-C3HC4; 1.

R SMART; SM00114; CARD: 1.

R SMART; SM00144; CARD: 1.

R SMART; SM00144; CARD: 1.

R SMART; SM00144; RING; 1.
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPESES PRELIMINARY; PRT; 602 AA.
OPESES;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS01282; BIR_REPEAT_1; PROSITE: PS50143; BIR_REPEAT_2; PROSITE: PS50209; CARD; 1. Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognai
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_Tax1D=10116;
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295
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                                                                                                                                                                                                                                                                                                          SIMEDSTILSDWINS-NKQKNKYDFSCELYRMSTYSTFPAGVPVSERSLARAGFYYTGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIIKGTVRTFLS
                                                                                                                         TYHMWPLTFLSPSELARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF
                                                                                                                                                                                                                                        DKYKCFCCGLMLDNWKLGDSPIQKHKQLYPSCSFIQNLVSAS-----LGSTSKNTS
                                                                                                                                                                                                                                                                                GTIKGTVRTFLS
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CDGGLRCWESGDDPWVEHAKWFPRCEYLIRIKGQEFVGQVQAGYPHLLEQLLSTSDSPED
                           CDGGLRCWESGDDPWVEHAKWFPRCEFLIRNKGQEFVDEIQGRYPHLLEQLLSTSDTTGE
                                                      LKDVGQFTSQYTVSNLSMQTHAARVRTFSTWPSSALVHPQELASAGFYYTGHSDDVKCFC
                                                                  LENSLE-TLRFSISNLSMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFC
                                                                                                              TYQTWPLSFLSPAELAKAGFYYTGPGDRVACFACGGKLSNWDRKDDPLSEHRRHFPSCPF
                                                                                                                                                                    TMPSGFAAS
                                                                                                                                                                                   PMRNSFAHSLSPTLEHSSLFSGSYSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFL
                                                                                                                                                                                                                          DKVKCFCCGLMLDNWKQGDSPIEKHRKLYPSCSFVQTLNPANSLEASPQPPLPSTA--TS
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                                                                                                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                                                                                                                                      Score 2185;
Pred. No. 3
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                            CC91385EEA62DE5A CRC64;
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                      ; DB 11;
3.4e-146;
hes 93;
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                                                                                                                                                                                                                                                                                                                                                                  Length 602;
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                                                                  Query Match 51.2%;
Best Local Similarity 62.4%;
Matches 328; Conservative 6
                                                                                                                                                                         Pfmm; PF000653; BIR; 3.

Pfum; PF00047; 19; 2.

SWART; SW00238; BIR; 3.

SWART; SW00218; CASC; 1.

SWART; SW00410; IGC2: 1.

SWART; SW0410; IGC2: 1.

SWART; SW00410; IGC2: 1.

SWART; SW00410; IGC2: 1.
                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001370: BIR.
InterPro: IPR003576: Caspase.
InterPro: IPR003593: ICE_p20.
InterPro: IPR003598: Ig_c2.
InterPro: IPR003500: Ig_like.
InterPro: IPR003000: Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van den Berghe H., Marynen P.;
"The apoptosis inhibitor gene API2 and a novel 18q gene, MLT, are recurrently rearranged in the t(11;18)(q21;q21)p6ssociated with mucosa-associated lymphoid tissue lymphomas.";
Blood 93:3601-3609(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-99272400; PubMed-10339464;

Dierlamm J., Baens M., Wlodarska I., Stefanova-Ouzounova

Hernandez J.M., Hossfeld D.K., De Wolf-Peeters C., Hageme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UNH1;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF123094;
HSSP; Q13490; 10
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01-JUN-2001
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1 (TrEMBLrel. 17,
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                                                                  Score 1678; DB 4;
Pred. No. 4.8e-110;
1; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                           Length 1140
                                                                  Indels
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                                                                                                                                                 Query Match
Best Local S
Matches 206
                                                                                                                                                                                                                                                                                               Pendleton C. N., Bargmann W. J., Waradarajan J., B
"The apoptosis inhibitor ch-IAP1 is a direct tra
v-Rel and c-Rel.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ da
EMBL; AF311289; A6462316.1; -.
InterPro; IPR001370, BIR.
InterPro; IPR001370, BIR.
Pfam; PF00653; BIR; 3.
PMART; SM00238; BIR; 3.
PROSITE; PS0148; BIR; REPEAT_1; 1.
PROSITE; PS0148; BIR REPEAT_2; 3.
NN_TER
324 324 326
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Q9DDN2;
Q1-MAR-2001
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. APOPTOSIS INHIBITOR CH-I Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria;
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                                                                                                                                                    Local Similarity 63.4 nes 206; Conservative
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                                                                                                 SIMEDSTILSDWTNSNKQ--KMKYDFSCELYRMSTYSTFPAGVPVSERSLARAGFYYTGV
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NDKYKCFCCGLMLDNWKLGDSPIQKHKQLYPSCSFIQNLVSA-SLG-ST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEHDIIKQKTQIPLQARELIDTILVKGNAAANIFKNCLKEIDSTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNAEDEIREEERERATEEKESRIKITVNPESKAVLAGQFVKLCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNAEDEKREEEKEKQAEEMASDDLSLIRKNRMAL----FQQLTCVLPILDNLLKANVINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | IIHEGPGESSSEDAVMMNTPVVKSALEMGFNRDLVKQTVQSKILTTGENYKTVNDIVSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CWESGDDPWVQHAKWFPRCEYLIRIKGQEFIRQVQASYPHLLEQLLSTSDSPGDENAESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTSRYTVSNLSMQTHAARFKTFFNWPSSYLVNPEQLASAGFYYVGNSDDVKCFCCDGGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETLRESISNLSMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTFLSPTDLAKAGFYYIGPGDRVACFACGGKLSNWEPKDNAMSEHLRHFPKCPFIENQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTFLSPSELARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPFLENSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THSULPGTENSGYFRGSYSNSPSNPVNSRANQDFSALMRSSYHCAMNNENARLLTFQTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHSLSPTLEHSSLFSGSYSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKVKCFCCGLMLDNWKRGDSPTEKHKKLYPSCRFVQSLNSVNNLEATSQPTFPSSYTNS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKVKCFCCGLMLDNWKLGDSPIQKHKQLYPSCSFIQNLVSA-SLGSTSKNTSP--MRNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIVENSIFLSNLMKSANTFELKYDLSCELYRMSTYSTFPAGVPVSERSLARAGFYYTGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  001 (TrEMBLrel. 16, 0001 (TrEMBLrel. 16, 10001 (TrEMBLrel. 17, 10001 (TREMBLREL 17, 10001)
                                                                                                                                                                                                                                                                             324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Eute
Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                             36567 MW; 5E2B89DEAE3733F3 CRC64.
                                                                                                                                                 34.7%; Score 1138.5;
63.4%; Pred. No. 1.24
tive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
(FRAGMENT).
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                                                                                                                                                    .5; DB 13;
1.2e-72;
hes 55; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
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                                                                                                                                                      Indels
                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.R. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
idae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504
                                                                                                                                                                                                      324;
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Query Match
Best Local S
Matches 173
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O88642:
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-MISTAR: TISSUE-OVARY, CORPUS LUTEUM;
STRAIN-MISTAR: TISSUE-OVARY, CORPUS LUTEUM;
STRAIN-MISTAR: TISSUE-OVARY, CORPUS LUTEUM;
Cloning and characterisation of an inhibitor of apopto;
(IAP) in the rat corpus luteum.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBLT, APOBLEO3, AAG23497.1;
EMBLT, APOBLEO3, AAG23497.1;
TEXTAREMENTAL TESTAREMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR001370; BIR.
Pfam; PP00653; BIR; 2.
SMART; SM00238; BIR; 2.
PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           088642
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                                                                                                                                                                                                                                                                                                             93 WKLGDSPIQKHKQLYPSCSFIQNLVSASLGSTSKNTSPMRNSFAHSLSPTLEHSSLFSGS 152
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                                                                                                                                   GPGDRVPCFACGGKLSNWEPNDDLLSEHRRHFPHCPFLENTSETQRFSVSNLSMQTHSAR
                                                                                                                                                    GPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPFLENSLETLRFSISNLSMQTHAAR
                                                                                                                                                                                                                                                 YSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWPLTFLSPSELARAGFYYI 212
                                                                                                                                                                                                                                                                                        WKQGDSPTEKHRQFYPSCSFVQTLLSGGLQSAAKNTSPAKSRFAHSL--PLEQ----GGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FCCDGGLRCWESGDDPWIEHAKWFP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FCCDGGLRCWESGDDPWVEHAKWFP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFLENSL-ETLRESISNLSMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPMRNSFAHSLSPTLEHSSLFSGSYSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEAR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ODKVKCFSCGLVLDNWQPGDNAMEKHKQVYPSCSFVQNMLSLNNLGLSTHSAFSPLVASN
                                                                            | MRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPW 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFVENLMRDQPSFNVSNVTMQTHEARVKTFINWPTRIPVQPEQLADAGFYYYGRNDDVKC
                                                       MRTFLYWPSSYLVQPEQLASAGFYYVDHNDDVKCFCCDGGLRCWEPGDDPW
                                                                                                                                                                                                              + HSSLPSNPLNSRAVEDF-SLRMNPCSYAMSTEEARFLSYSMWPLSFLSPAELGKAAFYYT
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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224 AA;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          224
25209 MW; 213A52534D5EB56A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     28.9%;
                                                                                                                                                                                                                                                                                                                                                                18; Score 945.5; DB 11; Length
18; Pred. No. 3.1e-59;
18; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                                                                                7;
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                                                                                                                                                                       272
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ID Q9EQ05
PRELIMINARY; PRT; 501 AA.
AC Q9EQ05;
DT 01-MAR-2001 (TYEMBLICEL. 16, Created)
DT 01-MAR-2001 (TYEMBLICEL. 17, Last sequence updat
DT 01-JUN-2001 (TYEMBLICEL. 17, Last annotation upd
DE INHIBITOR OF APOPTOSIS PROTEIN 3.

OC EMARYOCA; Metazoa; Chordata; Craniata; Vertebr
QC EMARYOCA; Metazoa; Chordata; Craniata; Vertebr
QC Mammalia; Eutheria; Rodentia; Sciurognathi; Mur
QX NCBL_TAXID-10116;
RN SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
RT Cloning, Characterization and regulation of an
RT PROTEIN in the rat corpus luteum.",
RL SUBMITTED (SEP-2000) to the EMBL/GenBank/DDBJ d
CC -:- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGE
DR InterPro; IPRO01370; BIR.
DR InterPro; IPRO01370; BIR.
DR FABM: PP00053; BIR.
DR FABM: PP00057; Zf-C38H44; 1.
DR SMART; SM00238; BIR; 3.
DR PFABM: PP00057; BIR, 3.
DR PROSITE; PS01403; BIR, REPEAT_1; 1.
DR PROSITE; PS0120; BIR, 3.
DR PROSITE; PS01403; BIR, REPEAT_1; 1.
DR PROSITE; PS01403; BIR, REPEAT_1; 1.
DR PROSITE; PS01403; BIR, GPT PETBERSEBIC5NO
SEQUENCE 501 AA; 56548 MW; 0973FBF28EBIC5NO
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Best Local Similarity
Matches 204; Conserv
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EMBL, AF304333; AAG41192.1;
InterPro; IPRO01370; BIR,
InterPro; IPRO01370; BIR,
Ffam; PF00633; BIR; 3.
Ffam; PF00637; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
FRANTS SMO0184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-WISTAR: TISSUE-OVARY:
Lareu R.R. Bradley C.K., Lacher M., Friis R.R., Dharma
"Cloning, characterization and regulation of an inhibit
protesh in the rat corpus luteum.";
submitted (SEP-2000) to the BMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegious (Rat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                      425
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539
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LFVDKNMKYIPTEDVSGLSLEEQLRRLQEERTCKVCMDKEVSVVFIPCGHLVVCQECAPS
                                                                                                                                        TTGENYKTVNDIVSALLNAEDEKREEEKEKQAEEMASDDLSLIRKNRMALFQQLTCVLPI 478
                                                                                                                                                                                                                                                                     GEGDKYKCFHCGGGLADWKPSEDPWEQHAKWYPGCKYLLDEKGQEYINNI-----HLTHS
                                                                                                                                                                                                                                                                                                         GRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQ 358
                                                                                                                                                                                                                                                                                                                                                                                   -----ENSLETLRESISNLSMOTHAARMRTFMYWPSSVPVQPEQLASAGFYYV 298
                                                                                                                                                                                                                                                                                                                                                                                                                         HLSPRELASAGLYYTGIDDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFFVLGRNVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLSPSELARAGEYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LDRPSETHADYL-----LRTGQVVDISDT-IYPRNPAMCSEEARLKTFQNWPDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSPTLEHSSLFSGSYSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWP-LT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOYGDSAVGRHRRISPNCRFINGFYFEN-GAT-QSTSPGIQNGQYKSENCVGNRNHFA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TINKDE---EFVEEFNRIKTFANFPSSSPVSASTLARAGFLYTGEGDTVQCFSCHAAVDR
                                                                                                                                                                                        LGESVVRTAEKT------PSVTKKIDDTIFQNPMVQEAIRMGFNEKDIKKTMEEKLQ 397
                                                                                                                                                                                                                              LLSTSDTTGEENADPPIIHFGPGESSSEDAVMMNTPVVKSALEMGFNRDLVKQTVQSKIL 418
                                                                                                                                                                                                                                                                                                                                                 RSESGYSSDRNFPNSTNSPR----NPAMAEYDARIVTFGTWLYS--VNKEQLARAGFYAL
                                                                          LDNLLKANVINKQEHDIIKQKTQIPLQARELIDTILVKGNAAANIFKNCLKEIDSTLYKN
                                                                                                                TSGSNYLSLEVLIADLVSAQKDNSQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 AA; 56548 MW; 0973FBF28E81C5A0 CRC64;
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                                      -------SQTSLQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 898.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 150; Indels 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8e-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
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an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501;
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f apoptosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
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                                      431
                                                                                                                424
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.4
Best Local Similarity 33.4
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel, 15, Created)
01-MAR-2001 (TrEMBLrel, 16, Last sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last sequence update)
01-JUN-2001 (TrEMBLrel, 17, Last annotation update)
INHIBITOR OF APOPTOGIS PROTEIN 3.
RAILUS DOTAGOS (RAL).
ENGREYOLS Metzoas Chordsta; Craniata; Vertebrata; Euteleostomi;
Rummalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
MCBI_TaxiD=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9EQ04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS01282; BIR_REPEAT_1; 1.
PROSITE: PS50143; BIR_REPEAT_2; 3.
Zinc-finger.
SEQUENCE 501 AA; 56578 MW; 486:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-OVARY;
                 359 LLSTSDTTGEENADPPIIHFGPGESSSEDAVMMNTPVVKSALEMGFNRDLVKQTVQSKIL 418
                                                                                  299
                                                                                                                                                                    178
                                                      292 GEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLDEKGQEYINNI-----HLTHS 346
                                                                                                                                                                                              198 FLSPSELARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPFL-----
                                                                                                                                                                                                                         129 ----LDRPSETHADYL-----LRTGQVVDISDT-IYPRNPAMCSEEARLKTFQNWPDYA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      599 LRKCPICRGII
                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                      33 NSNKQKMKYDFSCELYRMSTYSTFPAGVPVSERSLARAGFYYTGVNDKVKCFCCGLMLDN 92
                                                                                                                                                                                                                                                                                                        93 WKLGDSPIQKHKQLYPSCSFIQNLVSASLGSTSKNTSP------MRNSFAHS 138
                                                                      GRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQ 358
                                                                                                           RSESGVSSDRNFPNSTNSPR----NPAMAEYDARIVTFGTWLYS--VNKEQLARAGFYAL 291
                                                                                                                                       -----ENSLETLRFSISNLSMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYV 298
                                                                                                                                                                    HLSPRELASAGLYYTGIDDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFFVLGRNVNV 237
                                                                                                                                                                                                                                                 LSPTLEHSSLESGSYSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWP-LT 197
                                                                                                                                                                                                                                                                              WQYGDSAVGRHRRISPNCRFINGFYFEN-GAT-QSTSPGIQNGQYKSENCVGNRNHFA-- 128
                                                                                                                                                                                                                                                                                                                                     DTNKDE---EFVEEFNRLKTFANFPSSSPVSASTLARAGFLYTGEGDTVQCFSCHAAVDR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDKCPMCCTVI 487
LGESVVRTAEKT-----PSVTKKIDDTIFQNPMVQEAIRMGFNFKDIKKTMEEKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 AA; 56578 MW; 4863F69FF2E0C8CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KDISTEEQLRRLQEEKLCKICMDRNIAIVFVPCGHLVTCKQCAEA
                                                                                                                                                                                                                                                                                                                                                                                          27.4%; score 898.5; DB 11; Length 501; 33.4%; Pred. No. 1.8e-55; tive 84; Mismatches 150; Indels 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501 AA
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476
                                                                                                                                                                                              250
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	NPAMAEYDARIVTFGTWLYSVNKEQLARAGFYAL 2	38 RSESGVSSDRNFPNS	Db .
	SISNI,SMOTHAARMRTFMYWDSSVDVODEOLASAGFYYV 298	:	Ş
	PRELASAGLYYTGIDDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFFVLGRNVNV 237	178 HLSPRELASAGLYYTGIDDQV	Ър
	ACFACGGKLSNWEPKDDAMSEHRRHFPNCPFL 250	198 FLSPSELARAGFYYIGPGDRV	Qy
	LLRTGQVVDISDT-IYPRNPAMCSEEARPKTFQNWPDYA 177	:     -LDRPSETHADY	Db
	PLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWP-LT 197	139 LSPTLEHSSLFSGSYSSLSPN	Qy
	NGFYFEN-GAT-QSTSPGIQNGQYKSENCVGNRNHFA 128	73 WQYGDSAVGRHRRISPNCRFI	Db
	WKLGDSPIQKHKQLYPSCSFIQNLVSASLGSTSKNTSPMRNSFAHS 138	93 WKLGDSPIQKHKQLYPSCSF1	Qy
	EFVEEENRLKTFANFPSSSPVSASTLARAGFLYTGEGDTVQCFSCHAAVDR 72	16 DTNKDEEFVEEFNRLKTE	Db
	STFPAGVPVSERSLARAGFYYTGVNDKVKCFCCGLMLDN 92	ISNKQKMKY	οy
15:	; Score 896.5; DB 11; Length 496; ; Pred. No. 2.5e-55; 86; Mismatches 155; Indels 173; Gaps 15;	Query Match 27.48 Best Local Similarity 33.18 Matches 205; Conservative	Que Bes Mat
	MW; SEEF142AAECOB/98 CKC04;	SQ SEQUENCE 496 AA; 3611/ MW; 9BEF142AAEC3B/98 C	ž
		Zinc-finger.	K.W.
	AT_1; 1.	PROSITE: PS01282; BIR_REPE	D DR
		SMART; SM00184; RING; 1.	DR
		Pfam; PF00097; zf-C3HC4; 1	DR
	ing.	Pfam; PF00653; BIR; 3.	DR DR
	3 1	InterPro; IPRO01370; BIR.	DR
	STROTTE STATE STATES.	EMBL; AF183429; AAG22969.1	DR
	BING-TYPE TINCER	Submitted (SEP-1999) to the	RL
	d 3 Genes.";	"Cioning and Characterizate Apoptosis Protein 1, 2, and Ap	7 7 13 7
	of the tablibition of	Holcik M., Lefebvre C.A.,	RA
		[1] SECHENCE FROM N.A.	R R P
		NCBI_TaxID=10116;	0 X
	ta; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; C	38
	•	Rattus norvegicus (Rat).	SO
	t annotation	01-JUN-2001 (TremBirel, 17	D DT
	u,	01-MAR-2001 (TremBirel. 16	DI.
	h 4 fe	Q9ESFO;	a A
	PRT; 496 AA.	Q9ESF0 PRELIMINARY;	E C
		LT 10	SC
		477 VDKCPMCCTVI 487	DЪ
		599 LRKCPICRGII 609	Qy
	EQLERIQEEKI.CKICMDRNIAIVEVPCGHLVTCKQCAEA 476	432KDISTE	Db
	LEVDKNMKYIPTEDVSGLSLEEQLRRLQEERTCKVCMDKEVSVVFIPCGHLVVCQECAPS 598	539 LEVDKNMKYIPTEDVSGLSLE	Qy
	-SSQTSLQ	425	Вb
	TOIPLOARELIDTILVKGNAAANIFKNCLKEIDSTLYKN 538	479 LDNLLKANVINKQEHDIIKQKTQIPLQAR	Qy
	DNSQDE 424	398 TSGSNYLSLEVLIADLVSAQKDNSQDE	рь
	TTGENYKTVNDIVSALLNAEDEKREEEKEKQAEEMASDDLSLIRKNRMALFQQLTCVLPI 478	419 TTGENYKTVNDIVSALLNAED	Qy

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Query Match
Best Local S
Matches 134
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SEQUENCE
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SMART; SM0023B, BIR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2000 (TrEMBLrel. 17, Last anotation update)
101-UN-2001 (TrEMBLrel. 17, Last anotation update)
101-HIBITOR OF APOPTOSIS 1 (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9IA69;
                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou H., Lamont S.J.; Genetic variation among chicken lines and mammalian species
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BREED FAYOUMI; TISSUE-SPLEEN; Zhou H., Lamont S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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                                                                                     62
                                                                                                                                                                                                            Local Similarity
                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENDDYKCFCCDGGLRCWESGDPWCEIAKWPPRCEFLIRMKGQEFVDEIGGRYPHLEO 358
                                           RTEMYMPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRC 333
                                                                                    ADKVACFTCGGQLSNWEPKDNAMSEHRRHFPNCPFVENLMRDQPSFNVSNVTMQTHEARV
                                                                                                GDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPFLENSL-ETLRFSISNLSMQTHAARM 273
                                                                                                                                          SFPQDPVTTRAAEDLSHLRSKLHNPSMSTEEARLRTFHAWPLMFLSPTELAKAGLYYLGT 61
                                                                                                                                                           SLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWPLTFLSPSELARAGFYYIGP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDKCPMCCTVITFKQKIFM 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRKCPICRGIIKGTVRTFL 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SQTSLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDNLLKANVINKQEHDIIKQKTQIPLQARELIDTILVKGNAAANIEKNCLKEIDSTLYKN 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSGSNYLSLEVLIADLVSAQKDNSQDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGENYKTVNDIVSALLNAEDEKREEEKEKQAEEMASDDLSLIRKNRMALFQQLTCVLPI 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGESVVRTAEKT------PSVTKKIDDTIFQNPMVQEAIRMGFNFKDIKKTMEEKLQ 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLSTSDTTGEENADPPIIHFGPGESSSEDAVMMNTPVVKSALEMGFNRDLVKQTVQSKIL 418
                             KTFINWPTRIPVQPEQLADAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWIEHAKWFPRC
                                                                                                                                                                                                                                                                                                             PS01282; BIR_REPEAT_1;
PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                     197
197 AA;
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                     197
22602 MW;
                                                                                                                                                                                                24.5%; Score 801.5; DB 13 68.4%; Pred. No. 3.9e-49; ative 33; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                     D7923DABCF623E1A CRC64;
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                                                                                                                                                                                                                            DB 13; Length 197;
                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                  Gaps
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neograthae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                   09R015;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NEURONAL APOPTOSIS INHIBITORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF221082; AAF35319.1; -.
INTERPRO; IPRO01370; BIR.
Pfam; PF00653; BIR; 2.
SMART; SM00238; BIR; 2.
PROSITE; PS071282; BIR, REPEAT_1; 2.
PROSITE; PS50143; BIR_REPEAT_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou H., Lamont S.J.;
"Genetic variation among chicken lines "specific genes.";
"""" trans-John to the Funt GenBar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
11NIEBTOR OF APOPTOSIS (FRAGMENT).
                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BREED LEGHORN; TISSUE-SPLEEN
 MEDLINE-99431676; PubMed-10501978; Huang S., Scharf J.M., Growney J.E
                                                                                                                 BIRCIE OR NAIP
                                                                                                                                                                                                  Q9R015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                             SEQUENCE FROM N.A.
                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                  334
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182 EYLLRVKGGEFVSQVQ
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                                                                                                                                                                                                                                                                                                                                                         274
                                                                                                                                                                                                                                                                                                                                                                                     61 ADKVACFTCGGQLSNWEPKDNAMSEHRRHFPNCPFVENLMRDQPSFNVSNVTMQTHEARV
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                                                                                                                                                                                                                                                                                                                             EFLIRMKGQEFVDEI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                           SPPQDPVTTRAAEDLSHLRSKLHNPSMSTEEARLRTPHAWPLMFLSPAELAKAGLYYLGT
                                                                                                                                                                                                                                                                      EYLLRVKGGEFVSQV 195
                                                                                                                                                                                                                                                                                                                                                                                                               GDRVACEACGCKLSNWEPKDDAMSEHRRHFPNCPFLENSL-ETLRFSISNLSMQTHAARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWPLTFLSPSELARAGFYYIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 68.2
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195
195 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
22347 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 796.5; DB 1
Pred. No. 8.6e-49;
3; Mismatches 28
                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                  PRT;
   J.D.,
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   Endrizzi M.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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     Dietrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                      120
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ID QS
AC QS
AC QS
DT 01
DT 0
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Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP: 013450; B1rc1e.

MGD: MGZ:128220; B1rc1e.

HGD: MGZ:128220; B1rc1e.

InterPro; IPR001370; B1R.

Pram; PP00653; B1R; 3.

4 SMART; SM00238; B1R; 3.

8 PR0SITE; PS01282; B1R_REPEAT_2; 3.

PROSITE; PS01443; B1R_REPEAT_2; 3.

PROSITE; PS01443; B1R_REPEAT_2; 3.
                                                                                                                                                              09VUX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts.";
Mamm. Genome 10:1032-1035(1999).
EMBL; AF135493; AD56765.1; -.
HSSP: 013490; 10BH.
                                                                                                            01-MAY-2000
01-MAY-2000
   Drosophila melanogaster (Fruit fly)
                                                                               01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                            461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 DNWKLGDSPIQKHKQLYPSCSFIQNLVSASLGSTSKNTSPMRNSFAHSLSPTLEHSSLFS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 KMKYDFSCE------LYRMSTYSTFPAGVPVSERSLARAGFYYTGVNDKVKCFCCGCIML 90
                          GENE PRODUCT.
OR CG12284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KMKKGFNSQMRSEAKRLKTFETYDTFRSWTP---QEMAAAGFYHTGVRLGVQCFCCSLIL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPFLEN--SLETLRFSISNLSM
                                                                                                                                                                                                                                                                                                                                                                                    VSGLSLEEQLRRLQEERTCK 572
                                                                                                                                                                                                                                                                                                                                                                                                                                            VLTFHDILDDDSVIEIARAATSGGFQKLENLDISMNHKITEEGYRNFF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAQALGS --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QASEMASDDLSLIRKNRMALFQQLTCVLPILDNLL--KANVINKQEHDIIKQKTQIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSNCESLMAVLASCKKLREIEFSGRCFEAMTFVNILPNFVSLKILNLKDQQFPDKETSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --NRDLVKQTVQS-----KILTTGENYKTV-----NDIVSALLNAEDEK--REEEKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ALPEATETTRESNHGDAAAVH------STVVVKFIQNFPNLHVFHLKCDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEGLLSTSDTTGEEN-ADPPIIHFGPGESSSEDAVMMNTPVVKSA------LEMGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTGKKDIVRCFSCGGCLEKWAEGDDPMEDHIKFFPECVFLQTLKSSAEVIPTLQSQY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCEFLIRMKGQ-EFVDEIQGRYPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVHVTGEHFVKSWVRRELPMVSAYCNDSVFANEELRMDMFKDWPQESPVGVEALVRAGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTHAA------RMRTEMYWPSSVPVQPEQLASAGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYFTGKRDTYQCFSCGGSLGNWEEGDDPWKEHAKWFPKCEFLQSKKSSEEIAQYIQSYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G------KARYHE------EEARLESFEDWPFYNHGTSPRVLSAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSYSSLSPNPLNSRAVEDISSSRTNPYSYAMSTEEARFLTYHMWPLTF - - LSPSELARAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGNSLRKLPIERHKKLRPECEFLQGKDVGNIGK-----YDIRVKRPEKMLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LOARELI--DTILYKGNAANIFKNCLKEIDSTL-----YKNLFYDKNMKYIPTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163; Conserv
                                                                                                                                                                                                                                                                                                                                  -QALDNLPNLQELNICR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.1%;
ilarity 26.3%;
Conservative
                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                           PRELIMINARY;
                                                                                  13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LRNLEELLVPTGDGIHQVAKLIVRQCLQLPCLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78;
                                                                               Last sequence update)
Last annotation update)
                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 494; DB 11;
Pred. No. 8.1e-27;
78; Mismatches 197;
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4042E36E51A7F9A0 CRC64;
                                                                                                                                                                                               438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552
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                                                                                                                                                                                                                                                                                                                                                                                                                                            508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                SOW DER READ DE CONTRACTOR DE 
                                                    Ş
                                                                                                                В
                                                                                                                                                              8
   В
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00238; BIR; 2.
SMART; SM00184; RING; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00653; BIR; 2.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ballew
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                                                                                                                                                                                                                                                                                                                                                                                          Zincrfinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001370; BIR.
InterPro; IPR001841; Znf_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0003691; th.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                           218
                                                                                                                                                                                                                                                Local
   78
                                                                                                                22
                                                           VACFACGGKLSNWEPKDDAMSEHRRHFPNCPF--------LENSLETLRFSI-
   VKCFFCGVETGCWEQEDQPVPEHQRWSPNCPLLRRRTTNNVPINAEALDRILPPISYDIC
                                                                                                                                                                    NSRAVE----DISSSRTNPYSYAMSTEEARFLTYHMWPLTFLSPSELARAGFYYIGPGDR
                                                                                                                   NTNATQLFKNNINKTRMND-----LNREETRLKTFTDWPLDWLDKRQLAQTGMYFTHAGDK
                                                                                                                                                                                                                            127;
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                438 AA; 48038 MW;
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                   15.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Znf_ring
                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                       Score 490;
Pred. No.
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RA Besson K.Y., Bends P.V., Bermen B.P., Shandari D., Bollhakov S.R.
Ra Besson K.Y., Bends P.V., Bermen B.P., Shandari D., Bollhakov S.R.
Ra Cherry J.M., Cawley S., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Berriac C., Ferrica S., Fileischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
Davis M., Cawley S., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Carg N.S., Gelbart W.M., Glasser K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeysam C.,
RA Kimmel B.E., Kodica C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodica C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Helson M., Ketchum K.A.,
RA Hount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShreif A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Wisson K., Wusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski, N.P., Smith T.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski, N.P., Smith T.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski, N.P., Smith T.,
RA Shue B.C., Siden K.A., Wisson K.A., Weissenbach J.,
RA Yell S. Labo G., Siden K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLING-20196006; PubMed-10731132;
Adams M.D. Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D. Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pieiffer B.D.
Wan K.H., Doyle C., Baxeer E.G., Helt G., Nelson C.R., Miltos G.L.G
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkob C., Boldwin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Netazoa; Arthropoda; Tracheata; Haxapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso
Ephydroidea; prosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER EMBL; AE003528; AAG22319.1; -. HSSP; Q11490; 10BH.
                                                                                                     PROSITE; PS01282; BIR_REPEAT_1; PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M., Basu A., Baxendale J., Bayraktaroglu L.,
24CA8BC13F5DEF31 CRC64
                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.,
```

Mismatches

1e-26 DB 128; 5

Length 438 Indels

242;

Gaps

11;

137 261 77 217

```
C STRAIN-TRELAND;

A LAUZON H., AA1f B.M., Ladd T., Palli R.;

T "CCMNEV LAP gene.";

I SUDMITTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.

1. SUDMITTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: CONTAINS A RING-TYPE ZINC FINCER.

REMEL; U82310; AAD00537.1; -..

REMEL; U82310; AD00537.1; -..

REMEL; U82310; AD0053
                                                         Query Match
Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9YNL8;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                       Zinc-finger.
SEQUENCE 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choristoneura fumiferana nuclear polyhedrosis virus (CfMNPV). Viruses; dSDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus. Nucleopolyhedrovirus. NCBI_TaxID=10448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
181 MSTEEARFLTYHMWPLTFLSPSELARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 GANDSTLEMREHAYAEGVIPMSQLIQSIGMNAVNAAGSVTGTAAPQPRVTVATHASTATQ 197
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                                                         Local Similarity 24.5
nes 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCPLCRKPFTDVMRVYFS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCPICKGIIKGTVRTFLS 618
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                                                                                                                                                                                                       32090 MW;
                                                 14.8%; Score 486; DB 12;
24.5%; Pred. No. 1.1e-26;
tive 43; Mismatches 89;
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                                                                                                                                                                                                       B2D9BE8A359F105E CRC64;
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                                                     Indels 214;
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242 KIYCEYPCGHYVACGKCASSLTNCPICRYTYETAVRMY 279
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                                                                                               AAANI FKNCLKEIDSTLYKNLFVDKNMKY I PTEDVSGLSLEEOLRRLQEERTCKVCMDKE
                                                                                                                                                                SLIRKNRMALFQQLTCVLPILDNLLKANVINKQEHDIIKQKTQIPLQARELIDTILVKGN 518
                                                                                                                                                                                                 ALEMGFNRDLYKQTVQSKILTTGENYKTVNDIVSALLNAEDEKREEEKEKQAEEMASDDL 458
                                                                                                                                                                                                                                                                                                MKGQEFVDEIQGRYPHLLEQLLSTSDTTGEENADPPIIHFGPGESSSEDAVMMNTPVVKS 398
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                                                                                                                                                                                                                                                                                                                                                                                                  QKWAPQCPFLRRSGATLSAPQERAGLHAPQEREATNQLPSPPPAHPKYAIEAARLRTFTE 133
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